



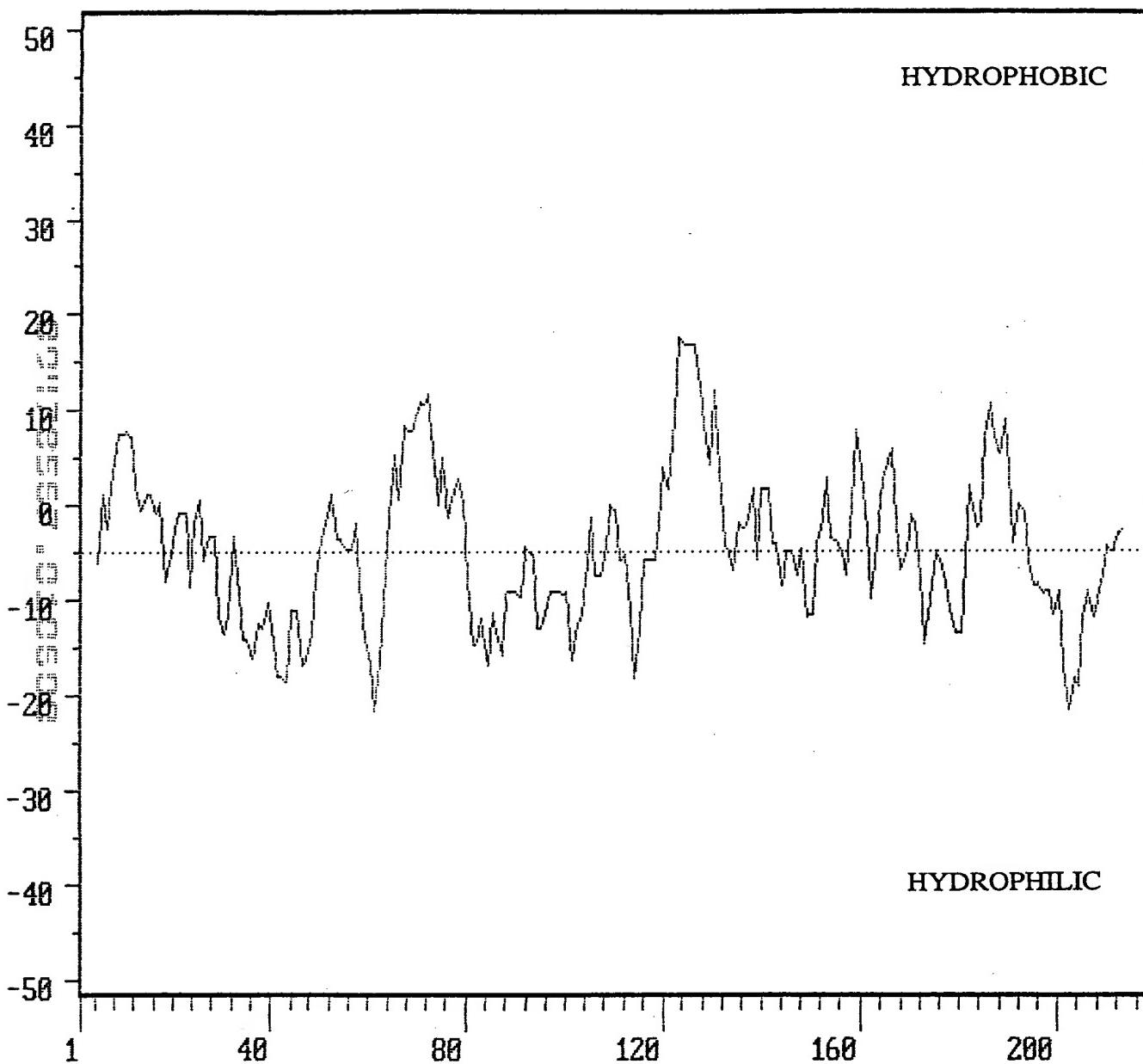
**Figure 2**

## PROPOSED VSP $\beta$ METHIONINE-ENRICHED VARIANTS

Fig. 3A

Hydropathy index computation for sequence VSPB.

Total number of amino acids is: 218.



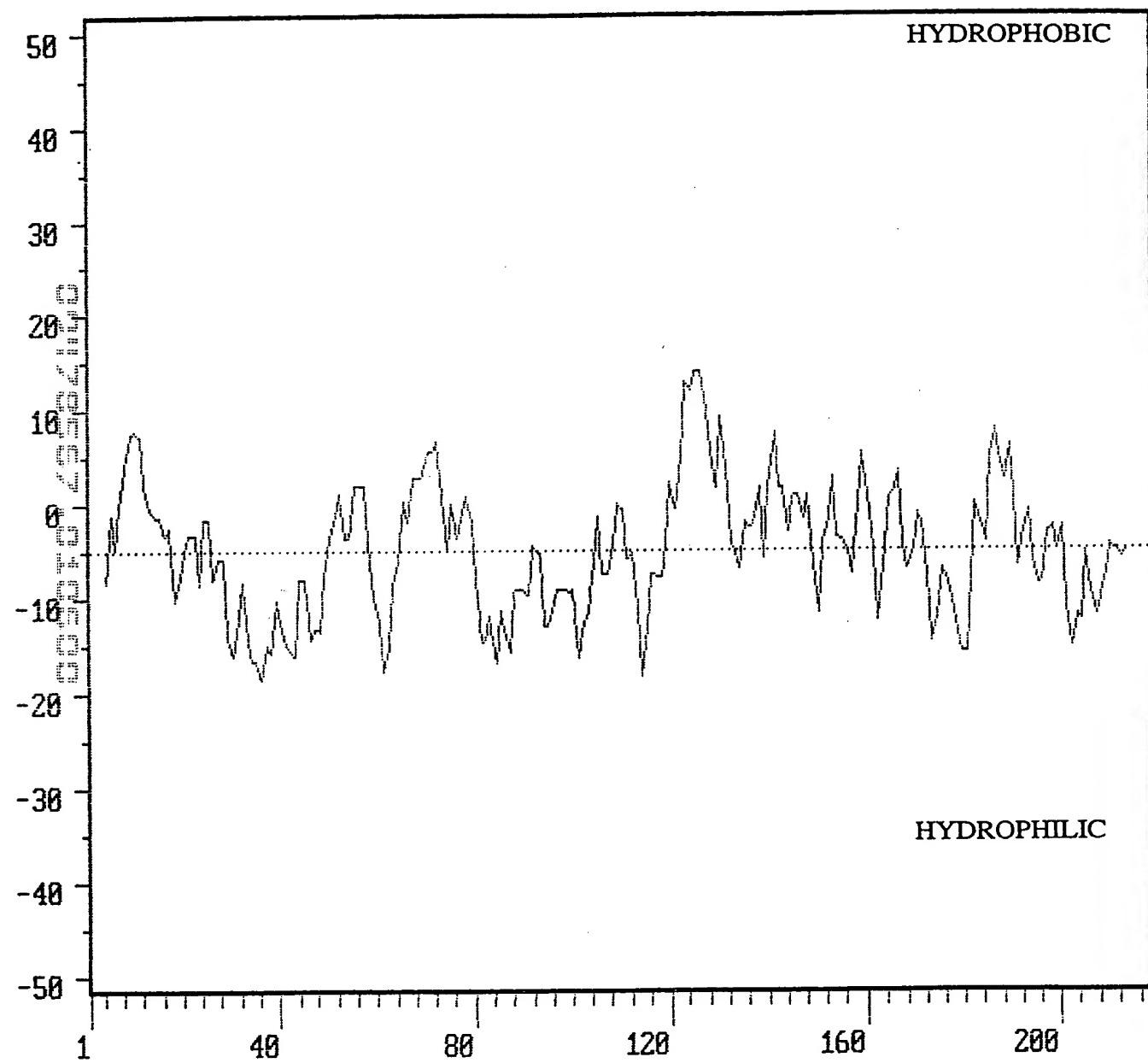
Hydropathic index of VSPB from amino acid 1 to amino acid 218.

Computed using an interval of 9 amino acids. (GRAVY = -4.95).

Fig. 3B

Hydropathy index computation for sequence VSPM10

Total number of amino acids is: 218.

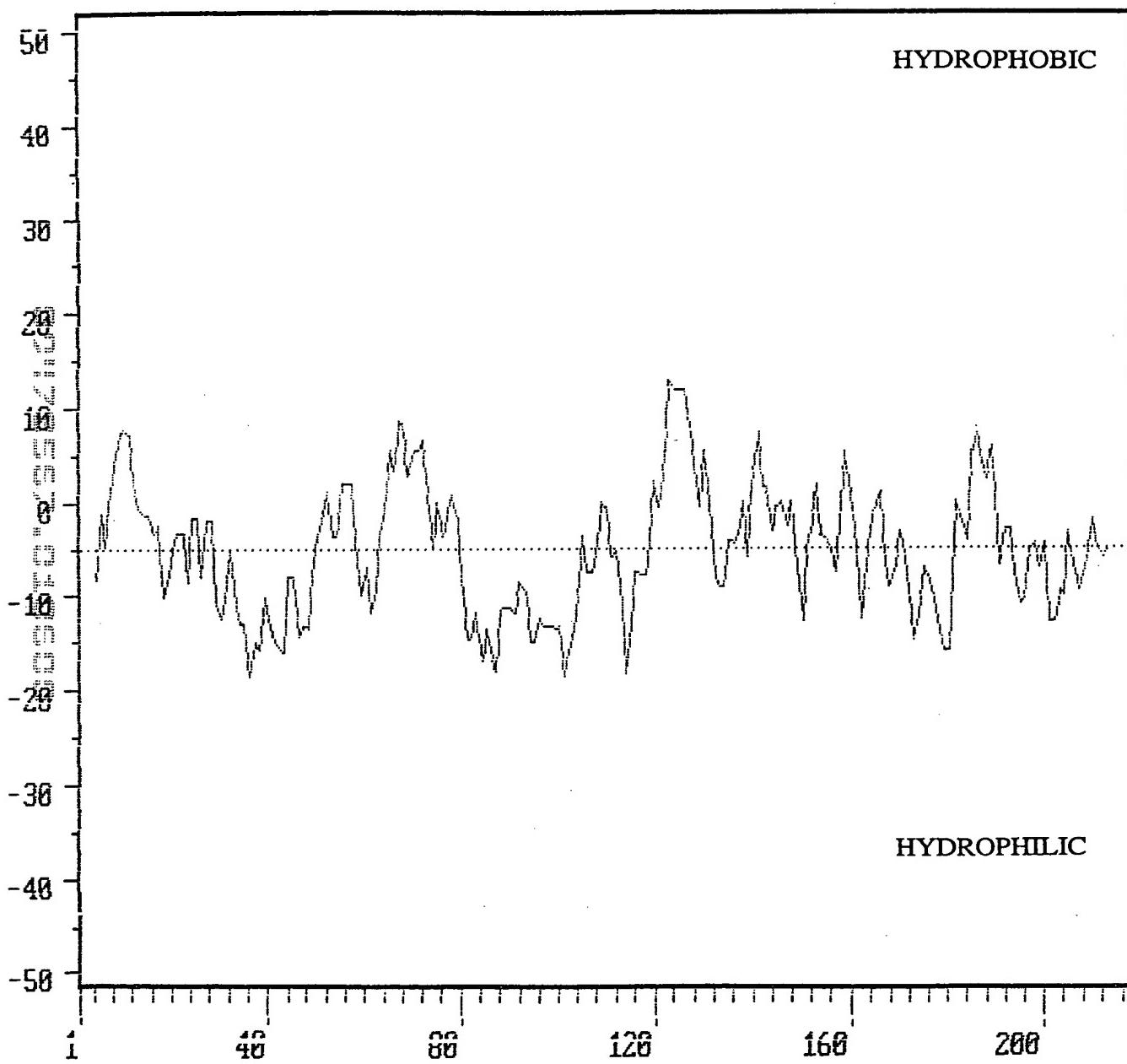


Hydropathic index of VSPM1 from amino acid 1 to amino acid 218.  
Computed using an interval of 9 amino acids. (GRAVY = -5.52).

Fig. 3C

Hydropathy index computation for sequence VSPM20.

Total number of amino acids is: 218.

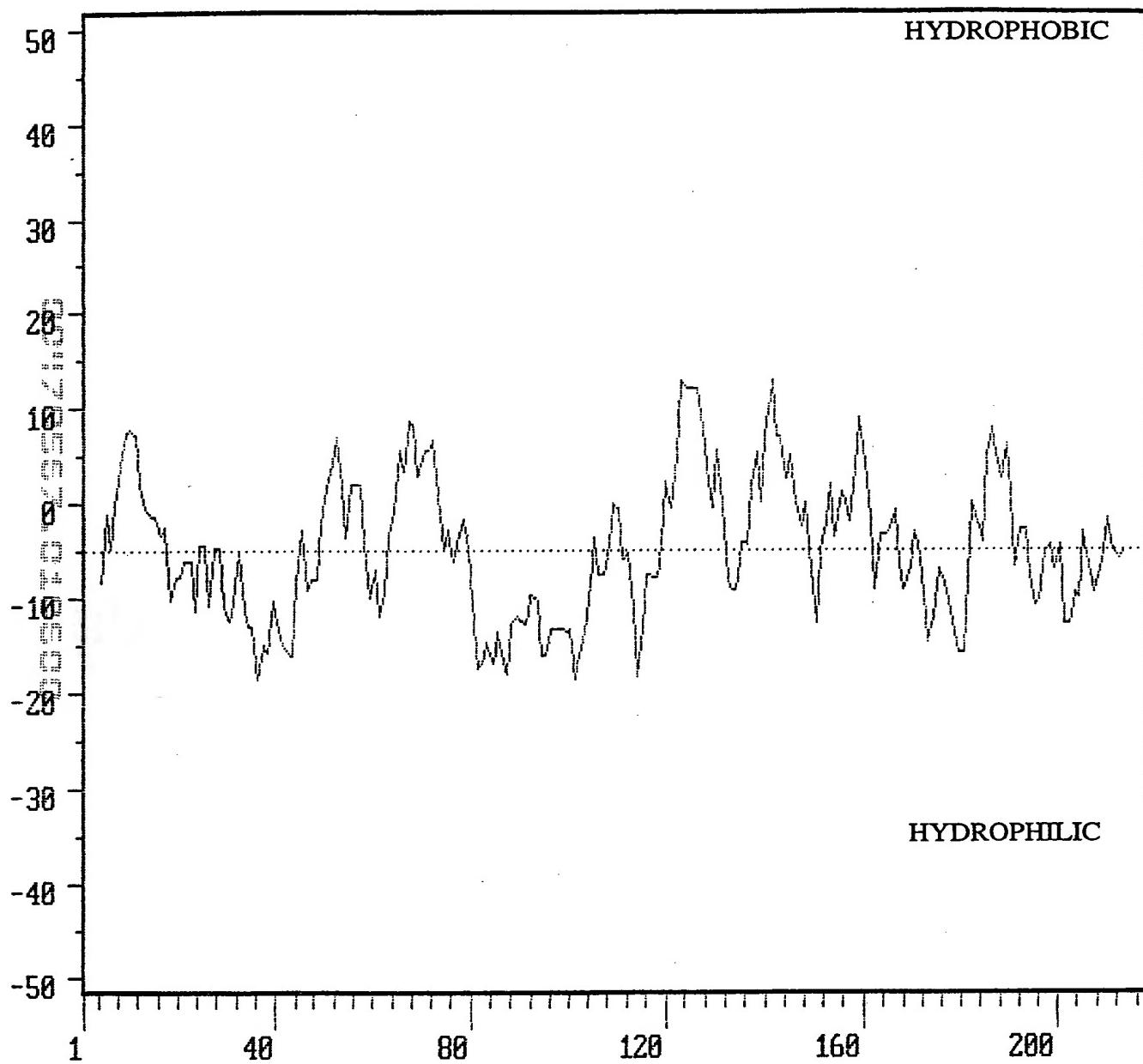


Hydropathic index of VSPM20 from amino acid 1 to amino acid 218.  
Computed using an interval of 9 amino acids. (GRAVY = -5.68).

Fig. 3D

Hydropathy index computation for sequence VSPM30.

Total number of amino acids is: 218.



Hydropathic index of VSPM30 from amino acid 1 to amino acid 218.

Computed using an interval of 9 amino acids. (GRAVY = -5.31).

Figure 4

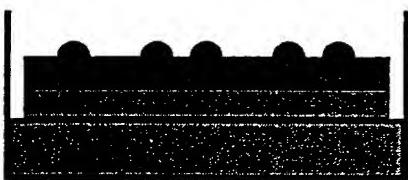
VSP $\beta$ -met10 sequence

**SfiI**

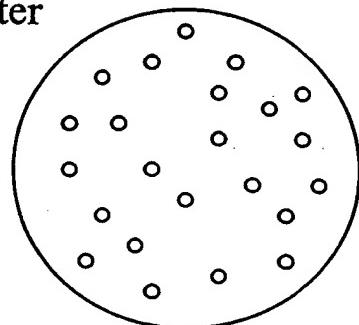
1	<u>GGCCCAGCCGGCCAGATCTCGGAGATGAAATGCGCTAGCTTAGGCTTGCTGTGGAAGC</u> CCGGGTGCGCCGGTCTAGAACGCTCTACCTTACCGCATCGAAATCCGAACGACACCTTCG	60
61	<u>ACACAACATGCGAGCCTTAAAACCATTCCCTGAAGAGTCATGGAACCAACAAAGGACTA</u> TGTGTTGACGCTCGAAATTTGTAAGGACTTCTCACGTACCTGGTTGTTCCCTGAT	120
121	<u>CATGAATGGCGAACAAATTCTGAATGGACTCTAAAACAGTTAACCAACAGGCCCTCTTTA</u> GTACTTACCGCTTGTAAAGCTTACCTGAGATTGTCATTGGTTGCCGAAGAAAAT	180
181	<u>TGCTAGTGAAATGAAATGCATCACAAACGACATGTTATTCGGCATGGATAACACCAT</u> ACGATCACTTACCTTACGTAGTGTGCTGTACAAATATAAGCCGTACCTATTGTGGTA	240
241	<u>GCTCTCTAATATCCCATACTATGAAAAACATGGATATGGGGTGGAGGAATTAAATGAAAC</u> CGAGAGATTATAGGGTATGATACTTTGTACCTATAACCCACCTCCTTAAATTACTTTG	300
301	<u>CTTATATGATGAATGGGTTAACAAAGGGCGACGCACCGCATTGCCAGAGACTCTTAAAAA</u> GAATATACTACTTACCCAATTGTTCCCGCTGCGTGGCCGTAACGGTCTCTGAGAATT	360
361	<u>TTACAAACAAGCTGATGTCCTTGGCTTCAAGATGGTATTCTGTCAGGAAGGTACCTTGA</u> AATGTTGTTGACTACAGGGAACCGAAGTTCTACCATAAGAACAGTCCTCCATGGAAC	420
421	<u>CAAAATGGCCGTAACAGAACCTAATGAAGGCTGGCTTCCACACATGGGAGCAGTT</u> GTTTACCGGCATTGTCTCGTTGGATTACTCCGACCGAACGGTGTACCTCGTCAA	480
481	<u>AATTCTCAAGGATCCACATCTTATGACTCCAAATGCACTTCATACAAATCAGCAATGAG</u> TTAAGAGTTCCCTAGGTGTAGAAACTGAGGTTACGTGAAAGTATGTTAGTCGTTACTC	540
541	<u>AGAGAATATGTTGAGGCAGGGATAACAGAATTGTTGAATGATTGGTGTCAATGGAGCGA</u> TCTCTTATACAACCTCCGTCCTATGTCTTAACAAACCTTACTAACCACTAGTTACCTCGCT	600
601	<u>TCTGCTTGGAGACACATGGCGAACATGAAACCTTAAAGCTTCAATCCCAGTACTA</u> AGACGAACCTCTGGTGTACCCGCTTAGATCTTGGAAATTGAAAGGATTAGGGTACATGAT	660
661	<u>CATGGAGGGCGGGCCG</u> 675 GTACCTCCGCCGGCG	

NotI

Figure 5  
Colony lift assay to detect protein-protein interactions



colonies on master filter  
VSP $\alpha$ -coated filter  
SB + amp + IPTG



Layer antigen (VSP $\alpha$ )-coated filter and  
colony lift filter on SB-IPTG-plate

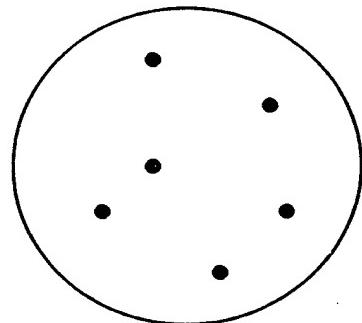
express VSP $\beta$  mutants at 30°C

master filter of colonies  
containing VSP $\beta$  mutants  
cloned into phagemid vecto

Correctly-folded VSP $\beta$  variants diffuse through  
the master filter and bind to the VSP $\alpha$ -coated filter

wash filter

VSP $\alpha$ -coated filter is incubated with  
HRP/anti-e tag conjugate



developed VSP $\alpha$ -  
coated filter

develop filter with substrate (ECL)